

CB



PCT10

#9

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/088,960

DATE: 01/30/2003
 TIME: 12:19:07

Input Set : A:\EP.txt
 Output Set: N:\CRF4\01302003\J088960.raw

3 <110> APPLICANT: Luo, Ying
 4 Mancebo, Halena
 6 <120> TITLE OF INVENTION: NOVEL SYK KINASE-ASSOCIATED CELL CYCLE PROTEINS,
 COMPOSITIONS, AND

7 METHODS OF USE

9 <130> FILE REFERENCE: A-68412-1/RMS/DHR
 11 <140> CURRENT APPLICATION NUMBER: US 10/088,960
 12 <141> CURRENT FILING DATE: 2002-03-22
 14 <150> PRIOR APPLICATION NUMBER: US 09/404,967
 15 <151> PRIOR FILING DATE: 1999-09-24
 17 <150> PRIOR APPLICATION NUMBER: PCT/US 00/26338
 18 <151> PRIOR FILING DATE: 2000-09-25

20 <160> NUMBER OF SEQ ID NOS: 12

22 <170> SOFTWARE: PatentIn version 3.1

24 <210> SEQ ID NO: 1

25 <211> LENGTH: 3955

26 <212> TYPE: DNA

27 <213> ORGANISM: Homo sapiens

29 <220> FEATURE:

30 <221> NAME/KEY: misc_feature

31 <222> LOCATION: (1473)..(1473)

32 <223> OTHER INFORMATION: "n" at position 1473 can be any base.

35 <400> SEQUENCE: 1

36 cggcagcaaa	ggaacgtgcg	aacgcgtgac	gccgccccgac	tggctcgccg	tctcccggtgc	60
38 cccggcgtcc	tccgccccgt	catggccccc	gccggccgg	acgagcggcg	ctgaggcg	120
40 cccggtggag	acgtgaggcg	gccggccgtgg	ccctcacagt	cggcgtttcg	ccgcctgccc	180
42 gccgtgccc	cgcacgcctg	ccgcccacatcg	cttcgcgcct	ggctggcg	ggcgcgtgtcc	240
44 tcccaggccc	tccgcgcgc	tccctggagc	tcggcggagc	gcggcagcca	gggcggcg	300
46 aggcgcgagg	agccggcg	caccggcg	gccggccg	ccggccgg	ggccatgacc	360
48 gtggagcaga	acgtgctgca	gcagagcgcg	gcccgcgc	accagcagac	gttttgaat	420
50 caactgagag	aaattacggg	gattaatgac	acccagatac	tacagcaagc	cttgaaggat	480
52 agtaatggaa	acttgaatt	agcagtggct	ttccttactg	cgaagaatgc	taagaccct	540
54 cagcaggagg	agacaactta	ctaccaaaca	gcacttcctg	gcaatgatag	atacatcagt	600
56 gtgggaagcc	aagcagatac	aaatgtgatt	gatctcactg	gagatgataa	agatgatctt	660
58 cagagaacaa	ttgcctttag	tttggccgaa	tcaaacaggg	cattcaggg	gacttggata	720
60 actgtatggag	aacaagccat	tagcagagtt	cttgaagcca	gtatagcaga	gaataaagca	780
62 tttttaaga	ggacacctac	agaagttgg	agggattctc	gaaaccctta	tgatagaaaa	840
64 agacaggaca	aagctccgt	tggctaaag	aatgttggca	atacttgg	gttttagtgct	900
66 gtattcagt	cattatcaa	tctttggaa	ttttagaagat	tagttctgaa	ttacaagcct	960
68 ccatcaaatg	ctcaagattt	accccgaaac	caaaaggaac	atcggattt	gcctttatg	1020
70 cgtgagctga	ggtatctatt	tgcacttctt	gttggtagcc	aaaggaagta	tggtgatcca	1080
72 tcaagagcag	ttgaaattct	taaggatgt	ttcaaatcaa	atgactcaca	gcagcaagat	1140
74 gtgagtgagt	ttacacacaa	attatttagat	tggttagaag	atgccttcca	aatgaaagct	1200
76 gaagaggaga	cggatgaaga	gaagccaaag	aacccatgg	taggtttagt	ctatggcaga	1260

P.6
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174 <220> FEATURE:
 175 <221> NAME/KEY: MISC_FEATURE
 176 <222> LOCATION: (373)..(373)
 177 <223> OTHER INFORMATION: "Xaa" at position 373 can be any amino acid.
 180 <400> SEQUENCE: 2
 182 Met Thr Val Glu Gln Asn Val Leu Gln Gln Ser Ala Ala Gln Lys His
 183 1 5 10 15
 186 Gln Gln Thr Phe Leu Asn Gln Leu Arg Glu Ile Thr Gly Ile Asn Asp
 187 20 25 30
 190 Thr Gln Ile Leu Gln Gln Ala Leu Lys Asp Ser Asn Gly Asn Leu Glu
 191 35 40 45
 194 Leu Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln
 195 50 55 60
 198 Glu Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr
 199 65 70 75 80
 202 Ile Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly
 203 85 90 95
 206 Asp Asp Lys Asp Asp Leu Gln Arg Thr Ile Ala Leu Ser Leu Ala Glu
 207 100 105 110
 210 Ser Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala
 211 115 120 125
 214 Ile Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu
 215 130 135 140
 218 Lys Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp
 219 145 150 155 160
 222 Arg Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn
 223 165 170 175
 226 Thr Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu
 227 180 185 190
 230 Phe Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp
 231 195 200 205
 234 Leu Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu
 235 210 215 220
 238 Leu Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val
 239 225 230 235 240
 242 Asp Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn
 243 245 250 255
 246 Asp Ser Gln Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp
 247 260 265 270
 250 Trp Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu
 251 275 280 285
 254 Glu Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu
 255 290 295 300
 258 Ala Val Gly Val Leu Glu Gly Lys Phe Glu Asn Thr Glu Met Phe
 259 305 310 315 320
 262 Gly Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys
 263 325 330 335
 266 Leu Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu
 267 340 345 350

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270 Asn Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Gly Leu Pro Pro
 271 355 360 365
W--> 274 Val Leu Thr Phe Xaa Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly
 275 370 375 380
 278 Arg Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr
 279 385 390 395 400
 282 Leu Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg
 283 405 410 415
 286 Glu Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg
 287 420 425 430
 290 Leu Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu
 291 435 440 445
 294 Val Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val
 295 450 455 460
 298 Cys Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly
 299 465 470 475 480
 302 Ser Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala
 303 485 490 495
 306 Leu Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile
 307 500 505 510
 310 Ser Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro
 311 515 520 525
 314 Pro Asp Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu
 315 530 535 540
 318 Leu Ser Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu
 319 545 550 555 560
 322 Asn Asp Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr
 323 565 570 575
 326 Ile Glu Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg
 327 580 585 590
 330 Leu His Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr
 331 595 600 605
 334 Trp Ala Tyr Ile Phe Asp His Arg Glu Ser Arg Trp Met Lys Tyr Asn
 335 610 615 620
 338 Asp Ile Ala Val Thr Lys Ser Ser Trp Glu Glu Leu Val Arg Asp Ser
 339 625 630 635 640
 342 Phe Gly Gly Tyr Arg Asn Ala Ser Ala Tyr Cys Leu Met Tyr Ile Asn
 343 645 650 655
 346 Asp Lys Ala Gln Phe Leu Ile Gln Glu Glu Phe Asn Lys Glu Thr Gly
 347 660 665 670
 350 Gln Pro Leu Val Gly Ile Glu Thr Leu Pro Pro Asp Leu Arg Asp Phe
 351 675 680 685
 354 Val Glu Glu Asp Asn Gln Arg Phe Glu Lys Glu Leu Glu Glu Trp Asp
 355 690 695 700
 358 Ala Gln Leu Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln
 359 705 710 715 720
 362 Lys Leu Arg Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly
 363 725 730 735
 366 Asp Pro Glu Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His

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367	740	745	750	
370	Leu Lys Glu Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His			
371	755	760	765	
374	Glu Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu			
375	770	775	780	
378	Tyr Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr			
379	785	790	795	800
382	Asp Tyr Arg Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Ala			
383	805	810	815	
386	Pro Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg			
387	820	825	830	
390	Asn Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln			
391	835	840	845	
394	Ala Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr			
395	850	855	860	
398	Glu Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr			
399	865	870	875	880
402	Leu Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser			
403	885	890	895	
406	Leu Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser			
407	900	905	910	
410	Lys Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg			
411	915	920	925	
414	Arg Glu Cys Leu Leu Lys Leu Asn Glu Gln Ala Ala Glu Leu Phe Glu			
415	930	935	940	
418	Ser Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile Ile Met Asn Glu			
419	945	950	955	960
422	Phe Ile Val Pro Phe Leu Pro Leu Leu Leu Val Asp Glu Met Glu Glu			
423	965	970	975	
426	Lys Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg Trp Cys Ser Tyr			
427	980	985	990	
430	Leu Gly Gln Glu Met Glu Pro His Leu Gln Glu Lys Leu Thr Asp Phe			
431	995	1000	1005	
434	Leu Pro Lys Leu Leu Asp Cys Ser Met Glu Ile Lys Ser Phe His			
435	1010	1015	1020	
438	Glu Pro Pro Lys Leu Pro Ser Tyr Ser Thr His Glu Leu Cys Glu			
439	1025	1030	1035	
442	Arg Phe Ala Arg Ile Met Leu Ser Leu Ser Arg Thr Pro Ala Asp			
443	1040	1045	1050	
446	Gly Arg			
447	1055			
450	<210> SEQ ID NO: 3			
451	<211> LENGTH: 4015			
452	<212> TYPE: DNA			
453	<213> ORGANISM: Homo sapiens			
455	<220> FEATURE:			
456	<221> NAME/KEY: misc_feature			
457	<222> LOCATION: (1473)..(1473)			
458	<223> OTHER INFORMATION: "n" at position 1473 can be any base.			

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/088,960

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1473
Seq#:2; Xaa Pos. 373
Seq#:3; N Pos. 1473
Seq#:4; Xaa Pos. 373
Seq#:5; Xaa Pos. 373

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:6,7